

SSPI

6358 TCATCAAAATATTTCACGACCATTCAGATTGGGTTCAATCAACAAGGTACGAGCCATATC
6417 ATGACGTTTATTAATTCCTGTAAGGTC TAACCCAAGTTAGTTGTTCCATGCTCGGTATAG
6418 ACTTTATTCAAAATTCGTTATCGCCAAAACCAAGAGAAGCACTCCCATCTCAAGGTTTGTA
6477 TGAATTAAGTTTAACTTACGGGTTTGTTCTTCCCTTGAGGGTAGGAGTTTCCAAACAT
6478 AGGAAGAAATTCCTCAGTCCAAGCCTCAACAAGGTCAGGTTACAGAGTCTCCAACCATTA
6537 TCCCTTCTTAAGAGTCAAGTTTCGGAGTTGTTCCAGTCCCATGTCTCAGAGGTTTGTAAT
6538 GCCAAAAGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAACACTACTGTTCAGCA
6597 CCGTTTTCGATGTCCTTACGTTACTTCTTGAAGTTAGTTTCATTTGATGACAAGGTCGT
6598 CATGCAATCATGGTTCAGTTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAGTTAGTGG
6657 GTACGTACGTACCAAGTCAATTCAAAGTCCTTTCTCTGTAAGTCGCTTCTGAATTTCAATCACC

Figure 1

SHEET 1 of 2

09137440 . 0820981599

6717

6777

6837

6897

5954

SHEET 2 of 2

509221 15-04-90

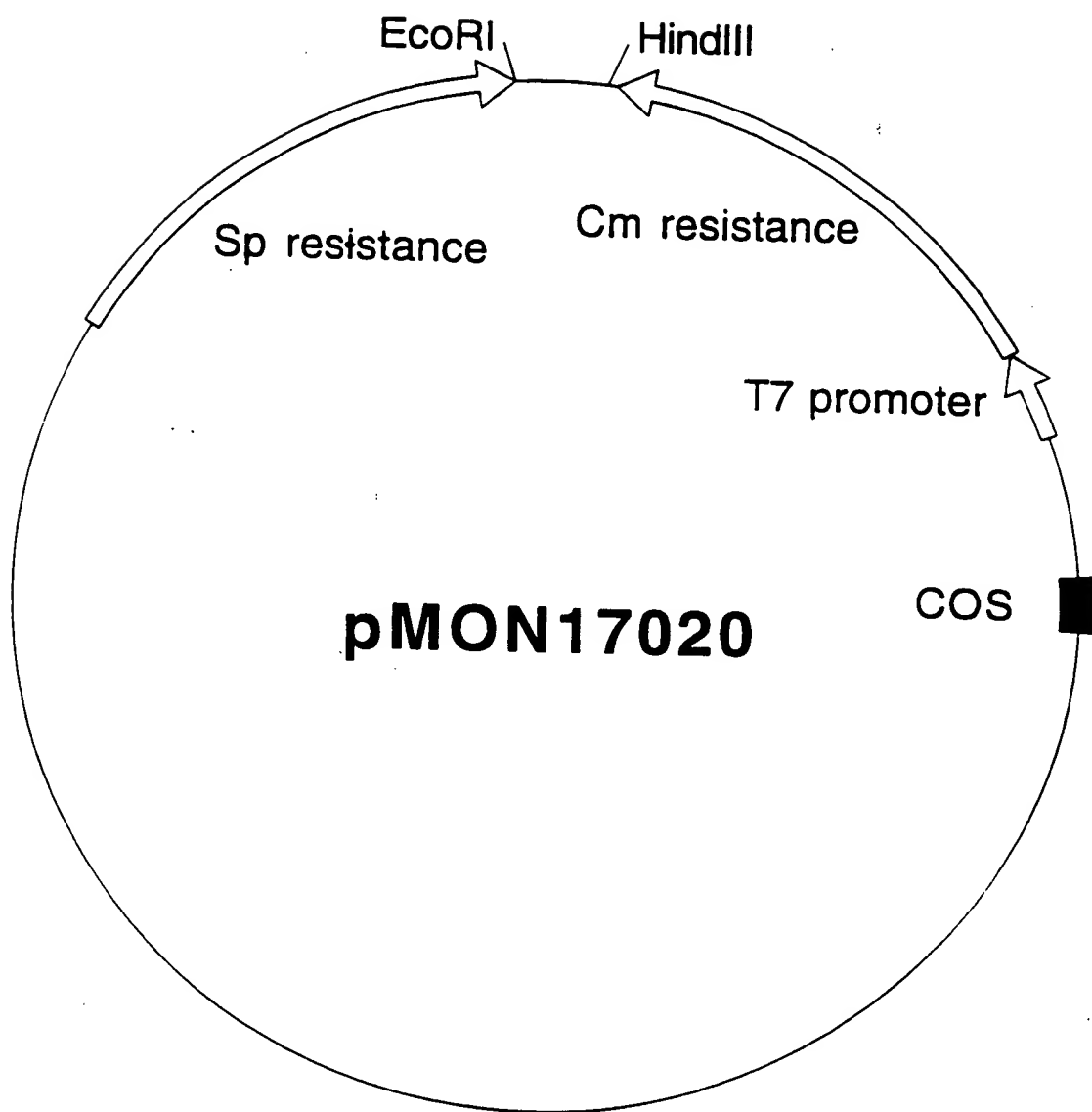


Figure 2

TTT GGC AAT GCC GCC ACC GGC TGC CGC CTG ACC ATG GGC CTC GTC GGC	394
Phe Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly	
100	105
110	
442	
GTC TTAC GAT TTC GAC AGC ACC TTC ATC GGC GAC GCC TCG CTC ACA AAG	
Val Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys	
115	120
125	
490	
CGC CCG ATG GGC CGC GTG TTG AAC CCG CTG CGC GAA ATG GGC GTG CAG	
Arg Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln	
130	135
140	
538	
GTG AAA TCG GAA GAC GGT GAC CGT CTT CCC GTT ACC TTG CGC GGC CCG	
Val Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro	
145	150
155	
586	
AAG ACG CCG ACG CCG ATC ACC TAC CGC GTG CCG ATG GCC TCC GCA CAG	
Lys Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln	
160	165
170	
175	
634	
GTG AAG TCC GCC GTG CTG CTC GCC GGC CTC AAC ACG CCC GGC ATC ACG	
Val Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr	
180	185
190	
682	
ACG GTC ATC GAG CCG ATC ATG ACG CGC GAT CAT ACG GAA AAG ATG CTG	
Thr Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu	
195	200
205	

Figure 3

004454099 1121599

ACC TTT CCG GAG TTT ATG GAC CTG ATG GCC GGG CTG GGC GCC AAG ATC	1402
Ser Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile	
435	
GAA CTC TCC GAT ACC AAG GCT GCC TGATGACCTT CACAATCGCC ATCGATGTC	1456
Glu Leu Ser Asp Thr Lys Ala Ala	
450 455	
CCGCTTCGCG CCGCAAGGG AGCTCTCGC GCCGTATCGC GGAGTCTAT GCTTTCATC	1516
ATCTTCGATTAC GGGCCCTGACC TATCGGCCCA CGGCCAAAGC GCTGCTCGAT CGCGGCTGT	1576
CGCTTCGATGA CGAGCGGCTT GCGGCCGATG TCGCCCGCAA TCTCGATCTT GCCGGGCTCG	1636
ACCGGTCGGT GCTGTGCGCC CATGCCATCG CGGAGCGGC TTCGAAGATC GCCGTCATGC	1696
CTTCGGTTCG GCGGGCGCTG GTCGAGCGGC AGCGCAGCTT TCGGGCGCGT GAGCCGGCA	1756
CGGTTCCTGGA TCGACGCCAT ATCGGCACGG TGGTCTGCC GGAATCGCCG GTGAAGCTCT	1816
ATGTCACCGC GTCACCGGAA GTGCGCGCA AACCGCGCTA TGACGAATC CTCGGCAATG	1876
GCGGCTTCG CGATTACGG ACGATCCTCG AGGATATCCG CCGCCGCGAC GAGCGGACA	1936
TGGGTCGGGC GGACAGTCCT TCGAAGCCCG CCGACGATGC GCACTT	1982

Figure 3

SHEET 5 of 5

0044099-101099

GTGAGGACGAC ATGATTACCTG TAGCTAGGAA GCCCGCTATC TCTCAATCCC GCGTGATCGC	60
GGGAGGAGTGT GACTGTGAAA AATCC ATG TCC CAT TCT GCA TCC CCG AAA CCA	112
Met Ser His Ser Ala Ser Pro Lys Pro	
1	5
GCA ACC GCC CGC CGC TCG GAG GCA CTC ACG GGC GAA ATC CGC ATT CCG	160
Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg Ile Pro	
10 15 20 25	
GGC GAC AAG TCC ATC TCG CAT CGC TCC TTC ATG TTT GGC GGT CTC GCA	208
Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu Ala	
30 35 40	
TCG GGC GAA ACC CGC ATC ACC GGC CTT CTG GAA GGC GAG GAC GTC ATC	256
Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile	
45 50 55	
AAT ACA GGC CGC GCC ATG CAG GCC ATG GGC GGC AAA ATC CGT AAA GAG	304
Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg Lys Glu	
60 65 70	
GGC GAT GTC TGG ATC ATC AAC GGC GTC GGC AAT GGC TGC CTG TTG CAG	352
Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu Leu Gln	
75 80 85	

Figure 4

00464099.121699

CAC ACC GAA AAG ATG CTG CAG GGC TTT GGC GCC GAC CTC ACG GTC GAG 736
 His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr Val Glu 210
 205 215

ACC GAC AAG GAT GGC GTG CGC CAT ATC CGC ATC ACC GGC CAG GGC AAG 784
 Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln Gly Lys 220
 225 230

CTT GTC GGC CAG ACC ATC GAC GTG CCG GGC GAT CCG TCA TCG ACC GCC 832
 Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser Thr Ala 235
 240 245

TTC CCG CTC GTT GCC GCC CTT CTG GTG GAA GGT TCC GAC GTC ACC ATC 880
 Phe Pro Leu Val Ala Ala Leu Leu Val Glu Gly Ser Asp Val Thr Ile 250
 255 260 265

GGC AAC GTG CTG ATG AAC CCG ACC CGT ACC GGC CTC ATC CTC ACC TTG 928
 Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu Thr Leu 270
 275 280

CAG GAA ATG GGC GAT ATC GAA GTG CTC AAT GCC CGT CTT GCA GGC 976
 Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu Ala Gly 285
 290 295

GGC GAA GAC GTC GCC GAT CTG CGC GTC AGG GCT TCG AAG CTC AAG GGC 1024
 Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu Lys Gly 300
 305 310

Figure 4

SHEET 3 of 5

109464099 . 121599

ATC GCC ACC TCC TTC CCC GAA TTC ATG GAC ATG ATG CCG GGA TTG GGC 1408
 Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly Leu Gly
 430 435 440

GCA AAG ATC GAG TTT AGC ATA CTC TAGTCAC TCG ACAGCGAAA TATTATTGCG 1462
 Ala Lys Ile Glu Leu Ser Ile Leu
 445

GAGATTGGGC ATTATTACCG GTTGGTCTCA GCGGGGTTT AATGTCCAAT CTTCATACG 1522

TTAACAGCATC AGGAAATATC AAAAAAGCTT TAGAAGGAAT TGCTAGAGCA GCGACGCCG 1582

CTAAGCTTTC TCAAGACTTC GTTAAACTG TACTGAATC CCGGGGGTC CGGGATCAA 1642

ATGACTTCTT TTTCTGAGAAA TTGGCCTCGC A 1673

Figure 4

SHEET 5 of 5

GTTGAATCGCGC CAAAAATGTGTA CTGTGAAAAA TCC ATG TCC CAT TCT GCA TCC CCG 54
 Met Ser His Ser Ala Ser Pro 1 5

AAA CCA GCA ACC GCC CGC CGC TCG GAG GCA CTC ACG GGC GAA ATC CGC 102
 Lys Pro Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg 10 15 20

ATT CCG GGC GAC AAG TCC ATC TCG CAT CGC TCC TTC ATG TTT GGC GGT 150
 Ile Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly 25 30 35

CTC GCA TCG GGC GAA ACC CGC ATC ACC GGC CTT CTG GAA GGC GAG GAC 198
 Leu Ala Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp 40 45 50 55

GTC ATC AAT ACA GGC CGC GCC ATG CAG GCC ATG GGC GCG AAA ATC CGT 246
 Val Ile Asn Thr Gly Arg Ala Met Glu Ala Met Gly Ala Lys Ile Arg 60 65 70

AAA GAG GGC GAT GTC TGG ATC ATC AAC GGC GTC GGC AAT GGC TGC CTG 294
 Lys Glu Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu 75 80 85

TTG CAG CCC GAA GCT GCG CTC GAT TTC GGC AAT GCC GGA ACC GGC GCG 342
 Leu Glu Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala 90 95 100

Figure 5 SHEET 1 of 5

Arg Leu Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe	390
105	110
ATC GGC GAC GCC TCG CTG TCG AAG CGC CCG ATG GGC CGC GTG CTG AAC	438
Ile Gly Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn	120
125	130
CCG TTG CGC GAA ATG GGC GTT CAG GTG GAA GCA GCC GAT GGC GAC CGC	486
Pro Leu Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg	140
145	150
ATG CCG CTG ACG CTG ATC GGC CCG AAG ACG ACG GCC AAT CCG ATC ACC TAT	534
Met Pro Leu Thr Leu Ile Gly Pro Lys Thr Ala Asn Pro Ile Thr Tyr	155
160	165
CCG GTG CCG ATG GCC TCC GCG CAG GTA AAA TCC GCC GTG CTG CTC GCC	582
Arg Val Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala	170
175	180
GGT CTC AAC ACG CCG GGC GTC ACC ACC GTC ATC GAG CCG GTC ATG ACC	630
Gly Leu Asn Thr Pro Gly Val Thr Thr Val Ile Glu Pro Val Met Thr	185
190	195
CGC GAC CAC ACC GAA AAG ATG CTG CAG GGC TTT GGC GCC GAC CTC ACG	678
Arg Asp His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr	200
205	210
215	

Figure 5

SHEET 2 of 5

GTC GAG ACC GAC AAG GAT GGC GTG CGC CAT ATC CGC ATC ACC GGC CAG	726
Val Glu Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln	
220	225
GGC AAG CTT GTC GGC CAG ACC ATC GAC GTG CCG GGC GAT CCG TCA TCG	774
Gly Lys Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser	
235	240
ACC GCC TTC CCG CTC GGT GCC GCC CTT CTG GTG GAA GGT TCC GAC GTC	822
Thr Ala Phe Pro Leu Val Ala Ala Leu Leu Val Glu Gly Ser Asp Val	
250	255
ACC ATC CGC AAC GTG CTG ATG AAC CCG ACC CGT ACC GGC CTC ATC CTC	870
Thr Ile Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu	
265	270
ACC TTG CAG GAA ATG GGC GCC GAT ATC GAA GTG CTC AAT GCC CGT CTT	918
Thr Leu Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu	
280	285
290	295
GCA GGC GGC GAA GAC GTC GCC GAT CTG CGC GTC AGG GCT TCG AAG CTC	966
Ala Gly Gly Glu* Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu	
300	305
310	
AAG GGC GTC GTC GGT CCG CCG GAA CGT GCG CCG TCG ATG ATC GAC GAA	1014
Lys Gly Val Val Val Pro Pro Glu Arg Ala Pro Ser Met Ile Asp Glu	
315	320
325	

Figure 5

TTC CCG GTC CTG GCG ATT GCC GCC TCC TTC GCG GAA GGC GAA ACC GTG 1062
 Tyr Pro Val Leu Ala Ile Ala Ala Ser Phe Ala Glu Gly Glu Thr Val 330 335 340

ATG GAC GGG CTC GAC GAA CTG CCG GTC AAG GAA TCG GAT CGT CTG GCA 1110
 Met Asp Gly Leu Asp Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala 345 350 355

GCG GTC GCA CGC GCG GTT GAA GCC AAC GCG GTC GAT TGC ACC GAA GGC 1158
 Ala Val Ala Arg Gly Leu Glu Ala Asn Gly Val Asp Cys Thr Glu Gly 360 365 370 375

GAG ATG TCG CTG ACG GTT CCG GCG CCG GAC GCG AAG GGA CTG GGC 1206
 Glu Met Ser Leu Thr Val Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly 380 385 390

GGC GGC ACG GTT GCA ACC CAT CTC GAT CAT CGT ATC GCG ATG AGC TTC 1254
 Gly Gly Thr Val Ala Thr His Leu Asp His Arg Ile Ala Met Ser Phe 395 400 405

CTC GTC ATG GCG CTT GCG GCG GAA AAG CCG GTG ACG GTT GAC GAC AGT 1302
 Leu Val Met Gly Leu Ala Ala Glu Lys Pro Val Thr Val Asp Asp Ser 410 415 420

AAC ATG ATC GCC ACG TCC TTC CCC GAA TTC ATG GAC ATG ATG CCG GGA 1350
 Asn Met Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly 425 430 435

Figure 5

SHEET 4 of 5

00464099-121699

TTG GGC GCA AAG ATC GAG TTG AGC ATA CTC TAGTCACTCG ACAGCGAAA 1400
Leu Gly Ala Lys Ile Glu Leu Ser Ile Leu
440 445

TATTAATTTGC GAGATTGGGC ATTATPACCG GTTGGTCTCA GCGGGGTTT AATGTCCAAT 1460
TATTCGATACG TAACAGCAATC AGGAAATATC AAAAAAGCTT 1500

248 TAFPLVAALIVGSDVTILNVLNPTRTGLILT..IQEMGADIEVINPRL 295
. | : : | | : : | : | : : : . | . : : : : : | : | | | . |
245 SASYFLA AAAA IKGGVKVTGIGRNSMOGDIRFADVLEKMGATI..... 287
200 AGGEDVALIKVKRSTLKGVTVPEDRAPSMIDEXPI LAVA AAF AEGATVMN 345
. | : | : : . : . | : : : : : : : | . : | . | | | . | : :
288 CWGDDY..IDGKGEINAI DMDMNHIP...DAAMT LATAALFAKGTTRLR 332
346 GLEELRVKESDKLSAVANGKLN GVDCEGETSLVVRGRPDGKGLGNASG 395
. : : : | | | | | | : : | : : | : . : : : | : : : : : : :
333 NIYNWRVKEPIDKL FAMA TELRKVGAEVEEGHDYIKI.TPPEKLN..... 376
396 AAVATHL DHR IAMSFLVMGLVSENPTVDDATMIATSPPEFMDLMAGLGA 445
| : : | | . | | | : | : | : : | : : | | : | : : : : : : : : : :
377 AEIATYNDHRMAINCFSVAL.SDTPVTILDPKCTAKTFFDYFEQLARISQ 425
446 KIELSDTKAA 456
426 AA^..... 428

Figure 6

SHEET 2 of 2

0004644090 121599

301 VADLRVRSSYLKGVTPVEDRAPSMIDEXPIILAVAAAFAGATVMNGLEEL 350
|||||.|.|||||.||.:|||||:|:|:|.|||.|||:|:|
301 VADLRVRASKIKGVVPPERAPSMIDEXPLAIAASFAGETVMDGLDEL 350
351 KVKESIDRLSAVANGLKINGVDCDEGETSLVVRGRPDGKGLNASGAAVAT 400
|||||.|||.|||.|||||.|||.||||| 1:|
351 KVKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPDGKGLG..GGTVAT 397
401 HLDHRIAMSEFVMGLVSENPVTVDDATMIATSEFVMDLMAGLAKIELS 450
|||||.|||||.|||.|||||.|||||.||:|:|
398 HLDHRIAMSEFVMGLAAEKPVTVDDSNMIATSEFVMDMPGLGAKIELS 447
451 DTRKAA* 456
448 LL.... 449

Figure 7

SHEET 2 of 2

0946409-194599

CCATGGCTTCA CGGTGCAAGC AGCCGTCACG CAACTGCTCG TTAAGTCCTCT GGTCTTTCTG	60
GAACCGTCCG TATTCCAGGT GACAAGTCTA TCTCCACAG GTCCCTTCATG TTTGGAGGTC	120
TGCGTACCGG TGAACCTCCG ATCACCGGTC TTTTGGAAGG TGAAGATGTT ATCAACACTG	180
GTAAAGGCTAT GCAAGCTATG GGTCCAGAA TCCGTAAGGA AGGTGATACT TGGATCATTG	240
ATTGCTGTGG TAACGGTGGG CTCTTGCTC CTGAGGCTCC TCTCGATTTC GGTAAACGCTG	300
CAACTGGTTG CCGTTTGACT ATGGGTCTTG TTGGTGTTTA CGATTTCGAT AGCACTTTCA	360
TTCGTGACCG TTCTCTCACP AAGCGTCCAA TGGGTCGTGT GTTGAACCA CTTCGCGAAA	420
TGCGTGTGCA GGTGAAGTCT GAAGACGGTG ATCGTCTTCC AGTTACCTTG CGTGAGCCAA	480
AGACTGCCAAC GCCAATCACC TACAGGGTAC CTATGGCTTC CGCTCAAGTG AAGTCCGCTG	540
TTCCTGCTTG TGGTCTCAAC ACCCCAGGTA TCACCACCTGT TATCGAGCCA ATCATGACTC	600
GTGACCTACAC TGAAAAGATG CTTCAGAGGTT TTGGTGCTTA CCTTACCCTT GAGACTGATG	660
CTTGACGCTGT GCGTACCATT CGTCTTGAGG GTCGTGGTAA GCTCACCGGT CAAGTGATTG	720
ATTGTTCAGG TGATTCATTG TCTACTGCTT TCCCATTTGG TGCTGCCCTTG CTTGTTCCAG	780
GTTCGGACGT CACCATCTTT AACGTTTGA TGAACCAAC CCGTACTGGT CTCATCTTGA	840

Figure 8

SHEET 1 of 2

09464099 121649

CTCTGCAGGA AATGGGTGTC GACATCGAAG TGATCAACCC ACGTCTTGCT GGTGAGAAG	900
ACGTGCCCTGA CTTCGGTGTTC CGTTCTTCTA CTTTGAAGGG TGTACTGTTC CCAGAAGACC	960
GTTCCTCCCTTC TATGATCGAC GAGTATCCA TTCTCGCTGT TGCAGCTGCA TTCGCTGAAG	1020
GTTCCTAACCGT TATGACACGGT TTGGAAGAAC TCCGTGTTAA GGAAGCGAC CGTCTTTCTG	1080
CTGTCCGCAAA CGGTCTCAAG CTCACGGGTG TTGATTGCCA TGAAGGTGAG ACTTCTCTCG	1140
TTCGTGCCGTGG TCGTCCCTGAC GGTAAAGGTC TCGGTAACGC TTCTGGAGCA GCTGTGCTA	1200
CCCACCTTGA TCACCGTATTC GCTATGAGCT TCCTCGTTAT GGGTCTCGTT TCTGA AAACC	1260
CTGTTACTGT TGAATGATGCT ACTATGATCG CTACTAGCTT CCCAGAGTTC ATGGATTTGA	1320
TGGCTGGTCT TGGAGCTAAG ATCGAACTCT CCGACACTAA GGCTGCTTGA TGAGCTC	1377

Figure 8

SHEET 2 of 2

09464095.121099

AGA TCT TTT TCA AGA	ATG GCA CAA ATT AAC AAC ATG GCT CAA GGG ATA CAA	49
	Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln	
	1	
	5	
	10	
ACC CTT AAT CCC AAT TCC AAT TTC CAT AAA CCC CAA GTT CCT AAA TCT		97
Thr Leu Asn Pro Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser		
15	20	25
TCA AGT TTT CTT GTT TTT GGA TCT AAA AAA CTG AAA AAT TCA GCA AAT		145
Ser Ser Phe Leu Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn		
30	35	40
TCT ATG TTG GTT TTG AAA AAA GAT TCA ATT TTT ATG CAA AAG TTT TGT		193
Ser Met Leu Val Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys		
45	50	55
		60
TCC TTT AGG ATT TCA GCA TCA GTG GCT ACA GCC TGC ATG C		233
Ser Phe Arg Ile Ser Ala Ser Val Ala Thr Ala Cys Met		
65	70	

Figure 11

AGATCTGCTA GAAATPAATTTT TGTTTAACTT TAAGAAGGAG ATATATCC ATG GCA CAA 57
 Met Ala Gln 1

ATT AAC AAC ATG GCT CAA GGG ATA CAA ACC CTT AAT CCC AAT TCC AAT 105
 Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro Asn Ser Asn 5 10 15

TTC CAT AAA CCC CAA GTT CCT AAA TCT TCA AGT TTT CTT GTT TTT GGA 153
 Phe His Lys Pro Gln Val Pro Lys Ser Ser Phe Leu Val Phe Gly 20 25 30 35

TCT AAA AAA CTG AAA AAT TCA GCA AAT TCT ATG TTG GTT TTG AAA AAA 201
 Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val Leu Lys Lys 40 45 50

09464099-124649

GAT	TCA	ATT	TTT	ATG	CAA	AAG	TTT	TGT	TCC	TTT	AGG	ATT	TCA	GCA	TCA	249
Asp	Ser	Ile	Phe	Met	Gln	Lys	Phe	Cys	Ser	Phe	Arg	Ile	Ser	Ala	Ser	
			55					60					65			

GTT	GCT	ACA	GCA	CAG	AAG	CCT	TCT	GAG	ATA	GTG	TTG	CAA	CCC	ATT	AAA	297
Val	Ala	Thr	Ala	Gln	Lys	Pro	Ser	Glu	Ile	Val	Leu	Gln	Pro	Ile	Lys	
		70					75					80				

GAG	ATT	TCA	GGC	ACT	GTT	AAA	TTG	CCT	GGC	TCT	AAA	TCA	TTA	TCT	AAT	345
Glu	Ile	Ser	Gly	Thr	Val	Lys	Leu	Pro	Gly	Ser	Lys	Ser	Leu	Ser	Asn	
		85				90					95					

AGA	ATT	C														352
Arg	Ile															
100																

Figure 12

09464099-121699

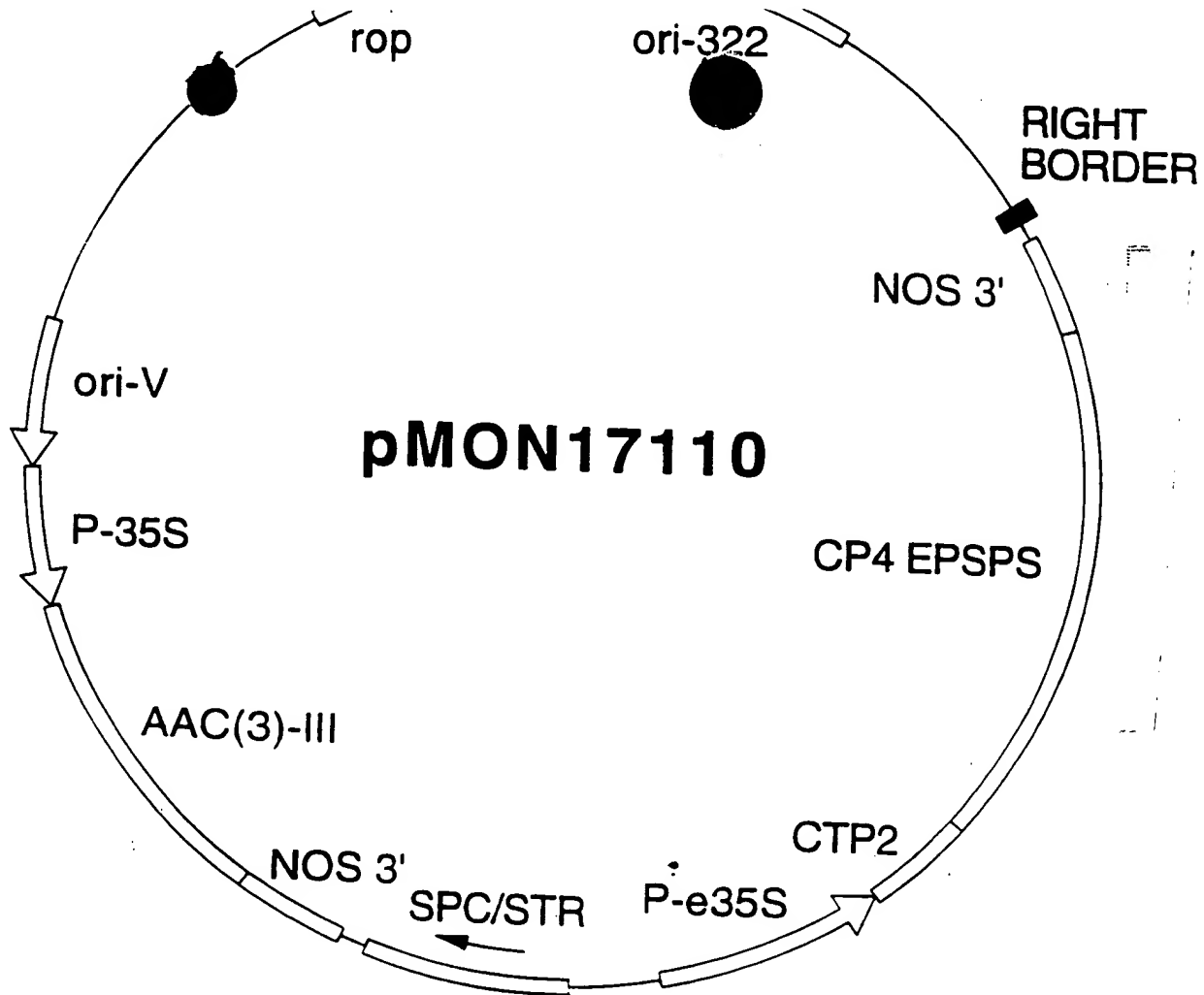


Figure 13

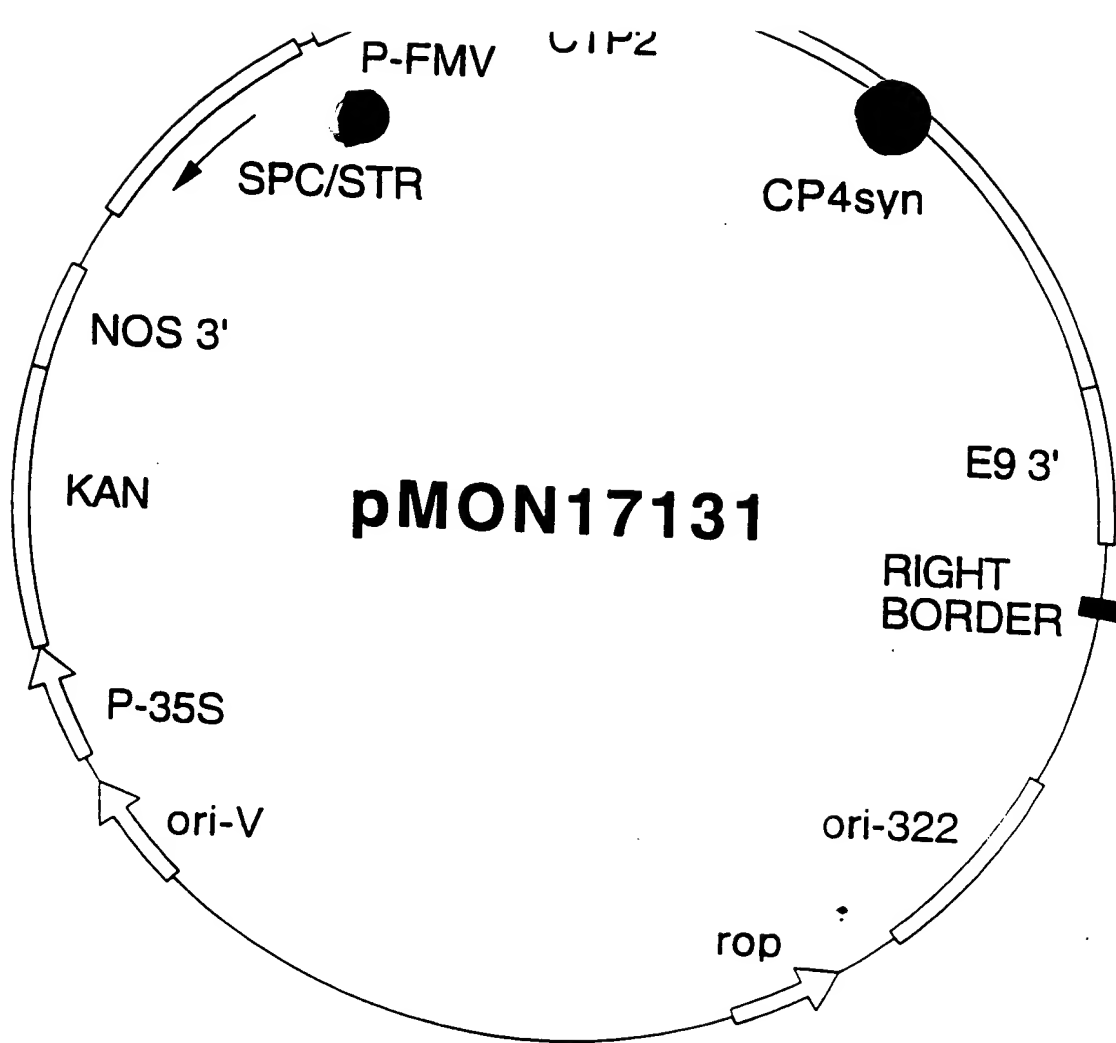


Figure 14

659121-65049160

6507960

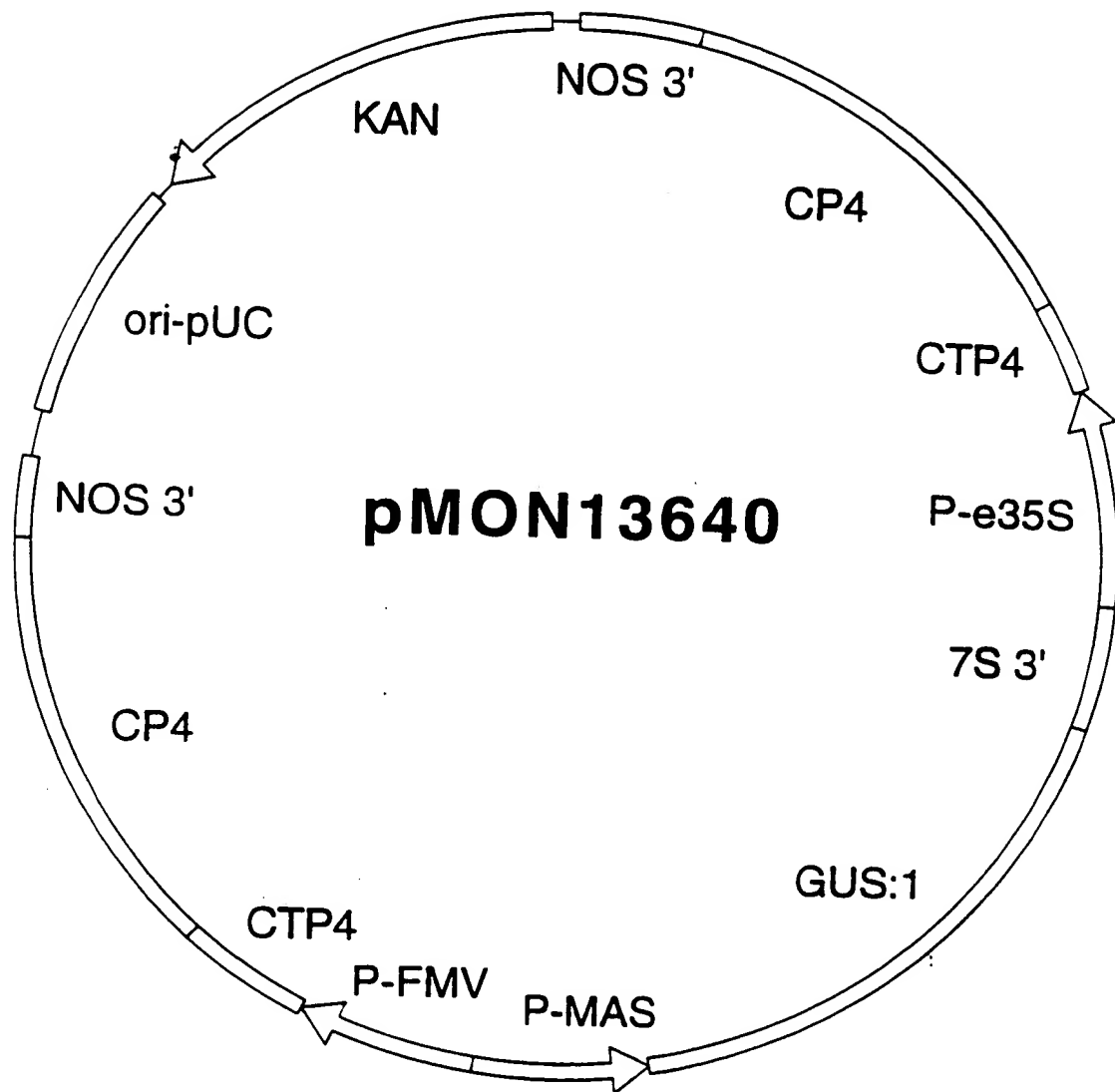


Figure 15

569727 66049460

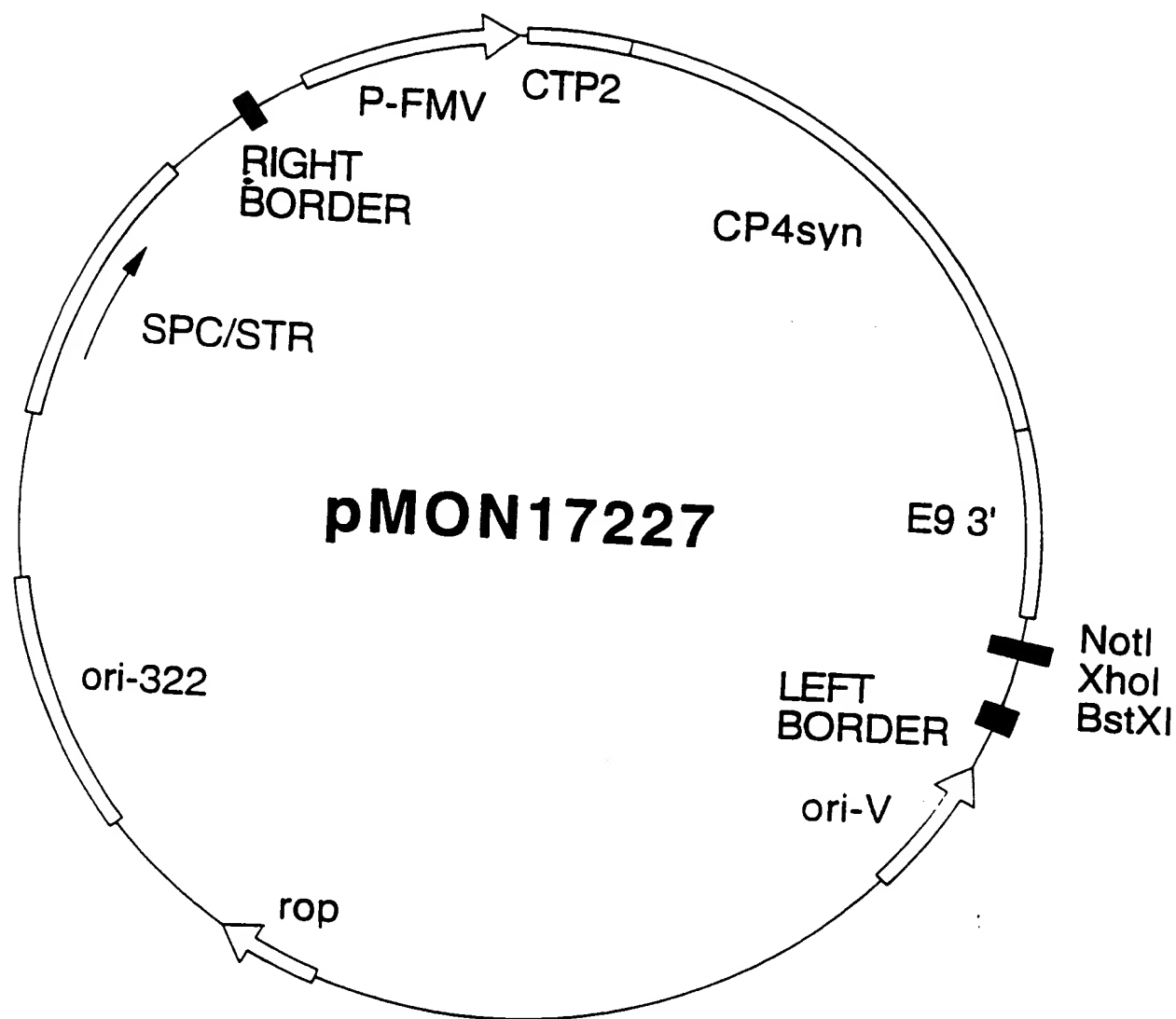


Figure 16

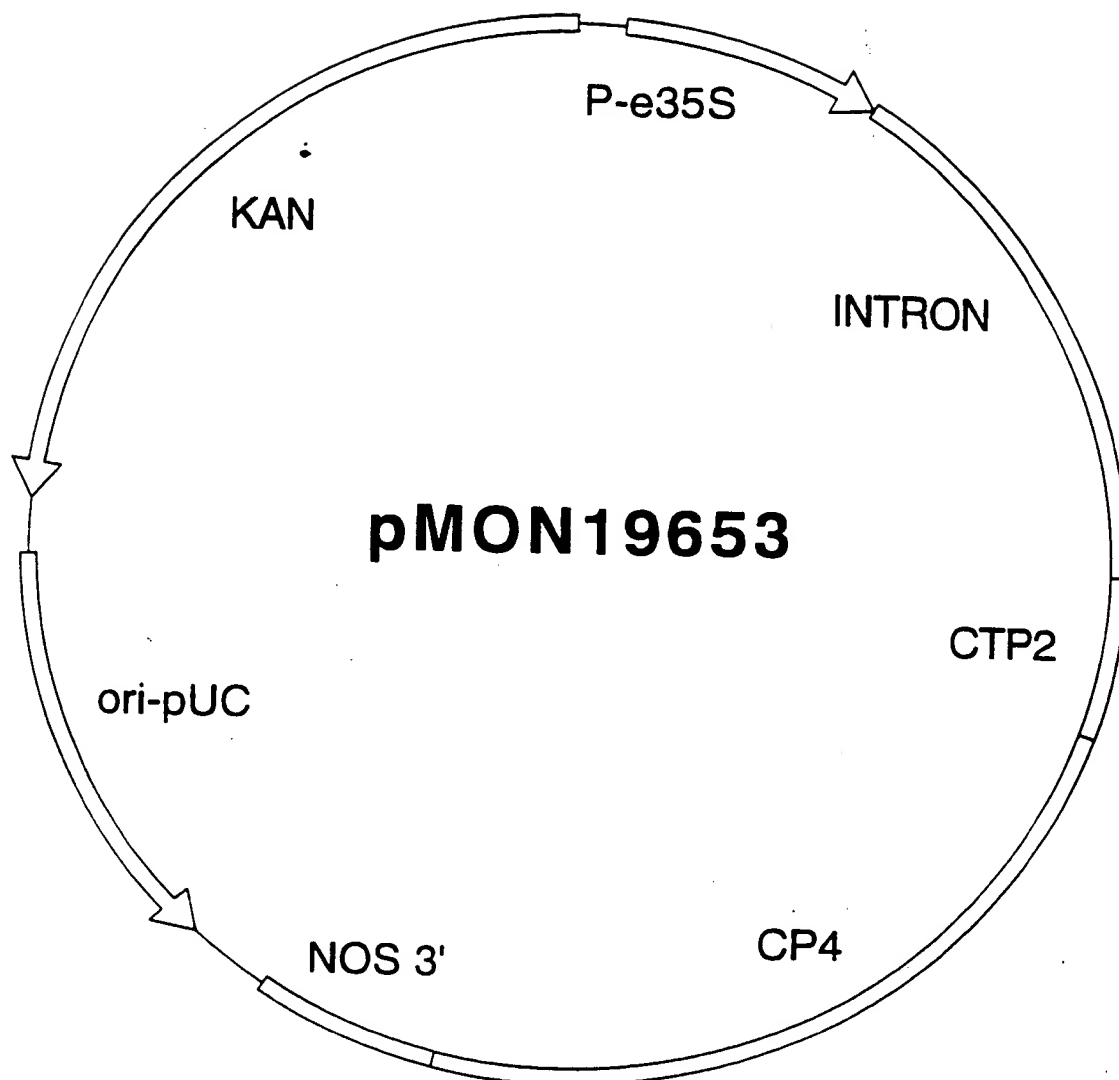


Figure 17

ATG AAA CGA GAT AAG GTG CAG ACC TTA CAT GGA GAA ATA CAT ATT CCC	48
Met Lys Arg Asp Lys Val Gln Thr Leu His Gly Glu Ile His Ile Pro	15
1	10
GGT GAT AAA TCC ATG TCT CAC CGC TCT GTT ATG TTT GGC GCG CTA GCG	96
Gly Asp Lys Ser Ile Ser His Arg Ser Val Met Phe Gly Ala Leu Ala	30
20	25
GCA GGC ACA ACA ACA GTT AAA AAC TTT CTG CCG GGA GCA GAT TGT CTG	144
Ala Gly Thr Thr Thr Val Lys Asn Phe Leu Pro Gly Ala Asp Cys Leu	45
35	40
ACG ACG ATC GAT TGC TTT AGA AAA ATG GGT GTT CAC ATT GAG CAA AGC	192
Ser Thr Ile Asp Cys Phe Arg Lys Met Gly Val His Ile Glu Gln Ser	60
50	55
AGC AGC GAT GTC GTG ATT CAC GGA AAA GGA ATC GAT GCC CTG AAA GAG	240
Ser Ser Asp Val Val Ile His Gly Lys Gly Ile Asp Ala Leu Lys Glu	80
65	70
CCA GAA AGC CTT TTA GAT GTC GGA AAT TCA GGT ACA ACG ATT CGC CTG	288
Pro Glu Ser Leu Leu Asp Val Gly Asn Ser Gly Thr Thr Ile Arg Leu	95
85	90
ATG CTC GGA ATA TTG GCG GGC CGT CCT TTT TAC AGC GCG GTA GCC GGA	336
Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly	110
100	105

Figure 18

GAT GAG AGC ATT GCG AAA CGC CCA ATG AAG CGT GTG ACT GAG CCT TTG	384
Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu	
115 120 125	
AAA AAA ATG GGG GCT AAA ATC GAC GGC AGA GCC GGC GAG TTT ACA	432
Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Glu Phe Thr	
130 135 140	
CCG CTG TCA GTG AGC GGC GCT TCA TTA AAA GGA ATT GAT TAT GTA TCA	480
Pro Leu Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser	
145 150 155 160	
CCT GTT GCA AGC GCG CAA ATT AAA TCT GCT GTT TTG CTG GCC GGA TTA	528
Pro Val Ala Ser Ala Gln Ile Lys Ser Ala Val Leu Leu Ala Gly Leu	
165 170 175	
CAG GCT GAG GGC ACA ACT GTA ACA GAG CCC CAT AAA TCT CGG GAC	576
Gln Ala Glu Gly Thr Thr Thr Val Thr Glu Pro His Lys Ser Arg Asp	
180 185 190	
CAC ACT GAG CGG ATG CTT TCT GCT TTT GGC GTT AAG CTT TCT GAA GAT	624
His Thr Glu Arg Met Leu Ser Ala Phe Gly Val Lys Leu Ser Glu Asp	
195 200 205	
CAA ACG AGT GTT TCC ATT GCT GGT GGC CAG AAA CTG ACA GCT GCT GAT	672
Gln Thr Ser Val Ser Ile Ala Gly Gln Lys Leu Thr Ala Ala Asp	
210 215 220	

SHEET 2 of 4

ATT	TPT	GTT	CCT	GGA	GAC	ATT	TCT	TCA	GCC	GGG	TTT	TTC	CTT	GCT	GCT	720
Ile	Phe	Val	Pro	Gly	Asp	Ile	Ser	Ser	Ala	Ala	Phe	Phe	Leu	Ala	Ala	240
225				230						235						
GGC	GGG	ATG	GTT	CCA	AAC	AGC	AGA	ATT	GTA	TTG	AAA	AAC	GTA	GGT	TTA	768
Gly	Ala	Met	Val	Pro	Asn	Ser	Arg	Ile	Val	Leu	Lys	Asn	Val	Gly	Leu	
				245					250					255		
AAT	CCG	ACT	CGG	ACA	GGT	ATT	ATT	GAT	GTC	CTT	CAA	AAC	ATG	GGG	GCA	816
Asn	Pro	Thr	Arg	Thr	Gly	Ile	Ile	Asp	Val	Leu	Gln	Asn	Met	Gly	Ala	
			260					265					270			
AAA	CTT	GAA	ATC	AAA	CCA	TCT	GCT	GAT	AGC	GGT	GCA	GAG	CCT	TAT	GGA	864
Lys	Leu	Glu	Ile	Lys	Pro	Ser	Ala	Asp	Ser	Gly	Ala	Glu	Pro	Tyr	Gly	
		275					280					285				
GAT	TTG	ATT	ATA	GAA	ACG	TCA	TCT	CTA	AAG	GCA	GTT	GAA	ATC	GGA	GGA	912
Asp	Leu	Ile	Ile	Glu	Thr	Ser	Ser	Leu	Lys	Ala	Val	Glu	Ile	Gly	Gly	
	290					295					300					
GAT	ATC	ATT	CCG	CGT	TTA	ATT	GAT	GAG	ATC	CCT	ATC	ATC	GCG	CTT	CTT	960
Asp	Ile	Ile	Pro	Arg	Leu	Ile	Asp	Glu	Ile	Pro	Ile	Ile	Ala	Leu	Leu	
305					310					315				320		
GGG	ACT	CAG	CCG	GAA	GGA	ACC	ACC	GTT	ATT	AAG	GAC	GCG	GCA	GAG	CTA	1008
Ala	Thr	Gln	Ala	Glu	Gly	Thr	Thr	Val	Ile	Lys	Asp	Ala	Ala	Glu	Leu	
				325					330					335		

Figure 18

AAA GTG AAA GAA	ACA AAC CGT ATT GAT ACT GTT GTT	TCT GAG	CTT CGC	1056
Lys Val Lys Glu	Thr Asn Arg Ile Asp	Ser Val Val	Glu Leu Arg	
340	345		350	
AAG CTG GGT GCT	GAA ATT GAA CCG ACA GCA GAT GGA	ATG AAG	GTT TAT	1104
Lys Leu Gly Ala	Glu Ile Glu Pro Thr Ala Asp Gly	Met Lys	Val Tyr	
355	360		365	
GGC AAA CAA ACG	TTC AAA GGC GCT GCA GTG TCC	AGC CAC	GGA GAT	1152
Gly Lys Gln Thr	Leu Lys Gly Gly Ala Ala Val Ser	Ser His	Gly Asp	
370	375		380	
CAT CGA ATC GGA	ATG ATG CTT GGT ATT GCT TCC	TGT ATA	ACG GAG	1200
His Arg Ile Gly	Met Met Leu Gly Ile Ala Ser	Cys Ile Thr	Glu Glu	
385	390		395	400
CCG ATT GAA ATC	GAG CAC ACG GAT GCC ATT CAC	GTT TCT	TAT CCA	1248
Pro Ile Glu Ile	Glu His Thr Asp Ala Ile His	Val Ser Tyr	Pro Thr	
405	410		415	
TTC TTC GAG CAT	TTA AAT AAG CTT TCG AAA AAA	TCC TGA		1287
Phe Phe Glu His	Leu Asn Lys Ser Leu Ser	Lys Lys		
420	425			

SHEET 4 of 4

ATG GTA AAT GAA CAA ATC ATT GAT ATT TCA GGT CCG TTA AAG GCC GAA	48
Met Val Asn Glu Gln Ile Ile Asp Ile Ser Gly Pro Leu Lys Gly Glu	
1 5 10 15	
ATA GAA GTG CCG GCC GAT AAG TCA ATG ACA CAC CGT GCA ATC ATG TTG	96
Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu	
20 25 30	
ATG TCG CTA GCT GAA GGT GTA TCT ACT ATA TAT AAG CCA CTA CTT GGC	144
Ala Ser Leu Ala Glu Gly Val Ser Thr Ile Tyr Lys Pro Leu Leu Gly	
35 40 45	
GAA GAT TGT CGT CGT ACG ATG GAC ATT TTC CGA CAC TTA GGT GTA GAA	192
Glu Asp Cys Arg Arg Thr Met Asp Ile Phe Arg His Leu Gly Val Glu	
50 55 60	
ATC AAA GAA GAT GAT GAA AAA TTA GTP GTG ACT TCC CCA GGA TAT CAA	240
Ile Lys Glu Asp Asp Glu Lys Leu Val Val Thr Ser Pro Gly Tyr Gln	
65 70 75 80	
GTP AAC ACG CCA CAT CAA GTA TTG TAT ACA GGT AAT TCT GGT ACG ACA	288
Val Asn Thr Pro His Gln Val Leu Tyr Thr Gly Asn Ser Gly Thr Thr	
85 90 95	
ACA CGA TTA TTG GCA GGT TTG TTA AGT GGT TTA GGT AAT GAA AGT GTP	336
Thr Arg Leu Leu Ala Gly Leu Leu Ser Gly Leu Gly Asn Glu Ser Val	
100 105 110	

Figure 19

AAA CCT GCA GAT TTT CAT GTT CCT GGC GAT ATT TCA TCT GCA GCG TTC	720
Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe	225
230	235
TTT ATT GTT GCA GCA CTT ATC ACA CCA GGA AGT GAT GTA ACA ATT CAT	768
Phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His	245
250	255
AAI GTT GGA ATC AAT CAA ACA CGT TCA GGT ATT ATT GAT ATT GTT GAA	816
Asn Val Gly Ile Asn Gln Thr Arg Ser Gly Ile Ile Asp Ile Val Glu	260
265	270
AAA ATT GGC GGT AAT ATC CAA CTT TTC AAT CAA ACA ACT GGT GCT GAA	864
Lys Met Gly Gly Asn Ile Gln Leu Phe Asn Gln Thr Thr Gly Ala Glu	275
280	285
CCT ACT GCT TCT ATT CCGT ATT CAA TAC ACA CCA ATG CTT CAA CCA ATA	912
Pro Thr Ala Ser Ile Arg Ile Gln Tyr Thr Pro Met Leu Gln Pro Ile	290
295	300
ACA ATC GAA GGA GAA TTA GTT CCA AAA GCA ATT GAT GAA CTG CCT GTA	960
Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val	305
310	315
ATA GCA TTA CTT TGT ACA CAA GCA GTT GGC ACG AGT ACA ATT AAA GAT	1008
Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp	325
330	335

Figure 19

SHEET 3 of 4

09464094.121549

GCG GAG GAA TTA AAA GTA AAA GAA ACA AAT AGA ATT GAT ACA ACG GCT 1056
 Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala 340 345 350

GAT ATG TTA AAC TTG TTA GGG TTT GAA TTA CAA CCA ACT AAT GAT GGA 1104
 Asp Met Leu Asn Leu Leu Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly 355 360 365

TTG ATP ATP CAT CCG TCA GAA TTT AAA ACA AAT GCA ACA GAT ATT TTA 1152
 Leu Ile Ile His Pro Ser Glu Phe Lys Thr Asn Ala Thr Asp Ile Leu 370 375 380

ACT GAT CAT CGA ATA GGA ATG ATG CTT GCA GTT GCT TGT GTA CTT TCA 1200
 Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser 385 390 395 400

ACC GAG CCG GTC AAA ATC AAA CAA TTT GAT GCT GTA AAT GTA TCA TTT 1248
 Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe 405 410 415

CCA GGA TTT TTA CCA AAA CTA AAG CTT TTA CAA AAT GAG GGA TAA 1293
 Pro Gly Phe Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly 420 425 430

Figure 19

SHEET 4 of 4

00464039-121599

PG2982	MSHSASPKPA	TARRSEALTG
LBAA	MSHSASPKPA	TARRSEALTG
Agrobacterium CP4	MSHGASSRPA	TARKSSGLSG
B. subtilis	M KRDKVQTLHG
S. aureus
S. cerevisiae
A. nidulans
B. napus
A. thaliana
N. tabacum
L. esculentum
P. hybrida
Z. mays
S. gallinarum
S. typhimurium
S. typhi
E. coli
K. pneumoniae
Y. enterocolitica
H. influenzae
P. multocida
A. salmonicida
B. pertussis
Consensus

Figure 20

00464099.121699

	PG2982	EIRIPGDKSI	SHRSFMFGCL	ASGETRITGL	LEGEDVINTG	RAMQAM.GAK	100
	LBAA	EIRIPGDKSI	SHRSFMFGGL	ASGETRITGL	LEGEDVINTG	RAMQAM.GAK	
Agrobacterium CP4		TVRIPGDKSI	SHRSFMFGGL	ASGETRITGL	LEGEDVINTG	KAMQAM.GAR	
B. subtilis		EIHIPGDKSI	SHRSVMFGAL	AAGTTVKNF	LPGADCLSTI	DCFRRM.GVH	
S. aureus		EIEVPGDKSM	THRAIMLASL	AEGVSTIYKP	LLGEDCRRTM	DIFRHL.GVE	
S. cerevisiae		VVIPGSKSI	SNRALILAAL	GEGQCKIKNL	LHSDDTKHML	TAVHELKAT	
A. nidulans		ICAPPGSKSI	SNRALVLAAL	GSGTCRIKNL	LHSDDTEVML	NALERLGAAT	
B. napus		LIKLPGSKSL	SNRILLLAAL	SEGTTVVDNL	LNSDDINMYL	DALKKL.GLN	
A. thaliana		LIKLPGSKSL	SNRILLLAAL	SEGTTVVDNL	LNSDDINMYL	DALKRL.GLN	
N. tabacum		TVKLPGSKSL	SNRILLLAAL	SKGRTVVDNL	LSDDDIHYML	GALKTL.GLH	
L. esculentum		TVKLPGSKSL	SNRILLLAAL	SEGRTVVDNL	LSDDDIHYML	GALKTL.GLH	
P. hybrida		TVKLPGSKSL	SNRILLLAAL	SEGTTVVDNL	LSSDDIHYML	GALKTL.GLH	
Z. mays		TVKLPGSKSL	SNRILLLAAL	SEGTTVVDNL	LNSDDVHYML	GALRTL.GLS	
S. gallinarum		AINLPGSKSV	SNRALLLAAL	ACGKTVLTNL	LDSDDVRRHML	NALSAL.GIN	
S. typhimurium		AINLPGSKSV	SNRALLLAAL	PCGKTALTNL	LDSDDVRRHML	NALSAL.GIN	
S. typhi		AINLPGSKSV	SNRALLLAAL	ACGKTVLTNL	LDSDDVRRHML	NALSAL.GIN	
E. coli		TINLPGSKTV	SNRALLLAAL	AHGKTVLTNL	LDSDDVRRHML	NALTAL.GVS	
K. pneumoniae		TVNLPGSKSV	SNRALLLAAL	ARGTTVLTNL	LDSDDVRRHML	NALSAL.GVH	
Y. enterocolitica		TVNLPGSKSV	SNRALLLAAL	AEGTTQNLNL	LDSDDIRHML	NALQAL.GVK	
H. influenzae		TINLPGSKSL	SNRALLLAAL	AKGTTKVTNL	LDSDDIRHML	NALKAL.GVR	
P. multocida		EVRLPGSKSL	SNRALLLSAL	AKGKTTLTNL	LDSDDVRRHML	NALKEL.GVT	
A. salmonicida		EVNLPGSKSV	SNRALLLAAL	ARGTTRLTNL	LDSDDIRHML	AALTQL.GVK	
B. pertussis		EVALPGSKSI	SNRVLLLAAL	AEGSTEITGL	LDSDDTRVML	AALRQL.GVS	
Consensus		PG-K--	R-----L	G-----L	D-----L		

Figure 20

09464997-121699

	101		150		
PG2982	IRKEGDVWII	NGVNGCLLQ	I.....EAA	LDFGNAGTGA	RLTMGLVGTY
LBAA	IRKEGDVWII	NGVNGCLLQ	P.....EAA	LDFGNAGTGA	RLTMGLVGTY
Agrobacterium CP4	IRKEGDTWII	DGVNGGLLA	P.....EAP	LDFGNAATGC	RLTMGLGVY
B. subtilis	IEQSSSDVVI	HKGIDALKE	P.....ESL	LDVNSGTTI	RLMLGILAGR
S. aureus	IKEDDEKLIV	TSPGYQ.VNT	P.....HQV	LYTGNSTTT	RLLAGLLSGL
S. cerevisiae	ISWEDNGETV	VVEGHG...	..STLSACADP	LYLGNAGTAS	RFLTSLAALV
A. nidulans	FSWEEEGEVL	VVNGKG...	..NLQASSSP	LYLGNAGTAS	RFLTVAATLA
B. napus	VERDSVNNRA	VVEGCGGIFP	ASLDSKSDIE	LYLGNAGTAM	RPLTAAVTAA
A. thaliana	VETDSENRA	VVEGCGGIFP	ASIDSKSDIE	LYLGNAGTAM	RPLTAAVTAA
N. tabacum	VEDDNENQRA	IVEGCGGQFP	VGKKSEEEIQ	LFLGNAGTAM	RPLTAAVTAA
L. esculentum	VEDDNENQRA	IVEGCGGQFP	VGKKSEEEIQ	LFLGNAGTAM	RPLTAAVTAA
P. hybrida	VEEDSANQRA	VVEGCGGLFP	VGKESKEEIQ	LFLGNAGTAM	RPLTAAVTAA
Z. mays	VEADKAAKRA	VVVGCGGKFP	VE.DAKEEVQ	LFLGNAGTAM	RPLTAAVTAA
S. gallinarum	YTL.SADRTTC	DITGNGGPLR	AP.....GALE	LFLGNAGTAM	RPLAAALCL.
S. typhimurium	YTL.SADRTTC	DITGNGGALR	AP.....GALE	LFLGNAGTAM	RPLAAALCL.
S. typhi	YTL.SADRTTC	DITGNGGPLR	AS.....GTLE	LFLGNAGTAM	RPLAAALCL.
E. coli	YTL.SADRTTC	EIINGGGLPH	AE.....GALE	LFLGNAGTAM	RPLAAALCL.
K. pneumoniae	YVLSADRTTC	EVTGTGGLQ	AG.....SALE	LFLGNAGTAM	RPLAAALCL.
Y. enterocolitica	YRLSADRTTC	EVDGLGKLV	AE.....QPLE	LFLGNAGTAM	RPLAAALCL.
H. influenzae	YQLSDDKTIC	EIEGLGAFN	IQ.....DNLS	LFLGNAGTAM	RPLTAALCLK
P. multocida	YQLSEDKSVC	EIEGLGRAFE	WQ.....SGLA	LFLGNAGTAM	RPLTAALCLS
A. salmonicida	YKLSADKTEC	TVHGLGRSFA	VS.....APVN	LFLGNAGTAM	RPLCAALCL.
B. pertussis	VGEVAD..GC	VTIEGVARFP	TE.....QAE	LFLGNAGTAF	RPLTAALALM
Consensus	-----	-----	-----	L--GN--T--	R-----

Figure 20

5-0

SHEET 5 of 11

[illegible]

251

Agrobacterium CP4

S. aureus

A. nidulans

A. thaliana

I. esculentum

2. mays

S. lymphimurium

E. coli

Y. entuercollitica

E. multirostris

B. *Derfusia*

Consensus

VIEPVMTRDH	TEKMLÖFGA	DI,I'VETDKD	VRHIRTÖG	KLVGÖ.TIDV	300
VIEPVMTRDH	TEKMLÖFGA	DI,I'VETDKD	VRHIRTÖG	KLVGÖ.TIDV	300

VTIRLEGRG KJTGQ VINDV

..INTTPEAI RYIKPADEHV

... ID. . VOKSTT EEHTYHIPOG BYVPAEVT

WDRFEVKGGO VS..VEHSDS

VEHSSG WDBEJVKGGO KVCSPKAAE

WDBEYTKGGO VK..AEHSDS

VE..IAN.HH YOOEVLKGGO OVHCBGVII

VE..IEN.OH YOOEVRKGGD SYOCDCSTVIT

VD.: VVH. EN YOTEHTKCCO

2008-09-09 10:10:10

ILISKPYIE ITLNLMARFG VS V PPDG WPAETLV

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

Figure 20

[illegible]

PG2982	PGDPSSTAFP	LVAALLVEGS	DVTIRNVLMN	PTRTGL...	I	LTLQEMGADI	350
LBAA	PGDPSSTAFP	LVAALLVEGS	DVTIRNVLMN	PTRTGL...	I	LTLQEMGADI	
Agrobacterium CP4	PGDPSSTAFP	LVAALLVPGS	DVTILNVLMN	PTRTGL...	I	LTLQEMGADI	
B. subtilis	PGDISSAAFF	LAAGAMVPNS	RIVLKNVGLN	PTRTGI...	I	DVLQNMGAHL	
S. aureus	PGDISSAAFF	IVAALITPGS	DVTIHNVGIN	OTRSGL...	I	DIVEKMGANI	
S. cerevisiae	ESDASSATYP	LAFAA.MTGT	TVTVPNIGFE	SLQGDARFAR		DVLKPMGCKI	
A. nidulans	ESDASCATYP	LAVAA.VTGT	TCTVPNIGSA	SLQGDARFAV		EVLKPMGCTV	
B. napus	EGDASSASYF	LAGAA.ITGE	TVTVEGCCGT	SLQGDVKFA.		EVLKMGCKV	
A. thaliana	EGDASSASYF	LAGAA.ITGE	TVTVEGCCGT	SLQGDVKFA.		EVLKMGCKV	
N. tabacum	EGDASSASYF	LAGAA.VTGG	TVTVEGCCGT	SLQGDVKFA.		EVLKMGAEV	
L. esculentum	EGDASSASYF	LAGAA.VTGG	TVTVEGCCGT	SLQGDVKFA.		EVLKMGAEV	
P. hybrida	EGDASSASYF	LAGAA.VTGG	TITVEGCCGTN	SLQGDVKFA.		EVLKMGAEV	
Z. mays	EGDASSASYF	LAGAA.ITGG	TVTVEGCCGT	SLQGDVKFA.		EVLKMGAKV	
S. gallinarum	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRK	SMQGDIFFA.		DVLEKMGATI	
S. typhimurium	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRK	SMQGDIFFA.		DVLEKMGATI	
S. typhi	EGDASSASYF	LAAGG.IKGG	TVKVTGIGGK	SMQGDIFFA.		DVLEKMGATI	
E. coli	EGDASSASYF	LAAA.IKGG	TVKVTGIGRN	SMQGDIFFA.		DVLEKMGATI	
K. pneumoniae	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRN	SVQGDIFFA.		DVLEKMGATV	
Y. enterocolitica	EGDASSASYF	LAAA.IKGG	TVRVGTIGKQ	SVQGDITKFA.		DVLEKMGAKI	
H. influenzae	EGDASSASYF	LAAGA.IK.G	KVKVTGIGKN	SIQGDRLFA.		DVLEKMGAKI	
P. multocida	EGDASSASYF	LAAA.IK.G	KVKVTGVGN	SIQGDRLFA.		DVLEKMGAKI	
A. salmonicida	EGDASSASYF	LAAGA.IK.G	KVRVTGIGKH	SI.GDIHFA.		DVLERMGARI	
B. pertussis	EGDASTASYF	LALGA.IGGG	PVRVTGVGED	SIQGDVAFFA.		ATLAAMGADV	
Consensus	D-S-----	-----	-----	-----	-----	MG----	

Figure 20

	PG2982	351	400
	LBAA		
Agrobacterium CP4	EVLNARLAGG	EDVADLRVR.	ASKLKGVVVP
B. subtilis	EVINPRLAGG	EDVADLRVR.	ASKLKGVVVP
S. aureus	EIKPSADSGA	EPYGDLLIE.	TSSLKAVEIG
S. cerevisiae	QL.FNQTTGA	EPTASIRIQY	TPMLQIPITIE
A. nidulans	...TQTATS	TTVSGRPV..	...GTLKPLK
B. napus	...EQTETS	TTVTGSPD..	...GILRATS
A. thaliana	...SWTENS	VTVTGSPRDA	FGMRHLRAV.
N. tabacum	...SWTENS	VTVTGPPRDA	FGMRHLRAI.
I. esculentum	...TWTEENS	VTVKGPPRNS	SGMKHLRAV.
P. hybrida	...TWTEENS	VTVKGPPRNS	SGMKHLRAI.
Z. mays	...TWTEETS	VTVTGPPREP	FGRKHLKAI.
S. gallinarum	...TWGDDF	I.....A	CTRGELHAI.
S. typhimurium	...TWGDDF	I.....A	CTRGELHAI.
S. typhi	...TWGDDF	I.....A	CTRGELHAI.
E. coli	...CWGDDY	I.....S	CTRGELNAI.
K. pneumoniae	...TWGEDY	I.....A	CTRGELNAI.
Y. enterocolitica	...SWGDDY	I.....E	CSRGELQGI.
H. influenzae	...TWGEDF	I.....Q	AEHAELNGI.
F. multocida	...TWGDDF	I.....Q	VEKGNLKI.
A. salmonicida	...TWGDDF	I.....E	AEQGPLHGV.
B. pertussis	...RYGPGW	IETRGVRAE	GGR..LKAF.
Consensus			

D-

Figure 20

	PG2982	101			450
	LBAA	AEG.....	ETVMDGLDEL	RVKESDRLAA	VARGLEANGV DCTEGEMSLT
Agrobacterium CP4		AEG.....	ETVMDGLDEL	RVKESDRLAA	VARGLEANGV DCTEGEMSLT
B. subtilis		AEG.....	ATVMNGLEEL	RVKESDRLSA	VANGLKINGV DCDEGETSLV
S. aureus		AVG.....	TSTIKDAEEL	KVKETNRIDT	VVSELRLKGA EIEPTADGMK
S. cerevisiae		SHSDPNSAN	TTTIEGIANQ	RVKECNRIILA	MATELAKFGV KTELPDGIQ
A. nidulans		HKPMEKSQTT	PPVSSGIANQ	RVKECNRIKA	MKDELAKEGV ICREHDDGLE
B. napus		ADG.....	PTTIRDVASW	RVKETERMIA	ICTELRKLGA TV.EEGSDYC
A. thaliana		ADG.....	PTTIRDVASW	RVKETERMIA	ICTELRKLGA TV.EEGSDYC
N. tabacum		ADG.....	PTAIRDVASW	RVKETERMIA	ICTELRKLGA TV.VEGSDYC
L. esculentum		ADG.....	PTTIRDVASW	RVKETERMIA	ICTELRKLGA TV.VEGSDYC
P. hybrida		ADG.....	PTAIRDVASW	RVKETERMIA	ICTELRKLGA TV.EEGPDYC
Z. mays		ADG.....	PTAIRDVASW	RVKETERMIA	IRTELTKLGA SV.EEGPDYC
S. gallinarum		AKG.....	TTTLRNINYNW	RVKETDRLFA	MATELRKVGA EV.EEGHDYI
S. typhimurium		AKG.....	TTTLRNINYNW	RVKETDRLFA	MATELRKVGA EV.EEGHDYI
S. typhi		AKG.....	TTTLRNINYNW	RVKETDRLFA	MATELRKVGA EV.EEGHDYI
E. coli		AKG.....	TTTLRNINYNW	RVKETDRLFA	MATELRKVGA EV.EEGHDYI
K. pneumoniae		ARG.....	TTTLRNINYNW	RVKETDRLFA	MATELRKVGA EV.EEGEDYI
Y. enterocolitica		ADG.....	PTVIRNINYNW	RVKETDRLSA	MATELRKVGA EV.EEGQDYI
H. influenzae		SNG.....	ETVIRNINYNW	RVKETDRLTA	MATELRKVGA EV.EEGEDFI
P. multocida		AEG.....	ETVIRNINYNW	RVKETDRLTA	MATELRKVGA EV.EEGEDFI
A. salmonicida		I,PR.....	VPHSQHLQL	AVRD.DRCTP	CTHGHRRÄQA GVSEEGTTFI
B. pertussis		ADG.....	PCRLRNIGSW	RVKETDRIHA	MHTELEKLGA GV.QSGADWL
Consensus			-V-----R-----		

Figure 20

ACGGGCTGTATA	ACGGTAGTAG	GGGTCCCGAG	CACAAAGCG	GTGCCGGCAA	GCAGACTAA	60
TTTCCATGGG	GAAATAATGCT	ATTTCATTGG	TTTGCCCTCT	GTCTGGCAA	TGGTTGCTAG	120
GGGATCCCT	GTTGAATTA	ACAACTGTC	GCCCTTCCAC	TGACCATGGT	AACGATGTT	180
TTTACTTCC	TGACTAACCG	AGGAAATTT	GGCGGGGGC	AGAAATGCCA	ATACAATTTA	240
GGTTGGTCTT	CCCTGCCCT	AATTGTCCC	CTCC	ATG	GCC TTG CTT TCC CTC	292
				Met	Ala Leu Leu Ser Leu	
				1	5	
AAC AAT CAT CAA	TCC CAT CAA	CGC TTA	ACT GTT	AAT CCC	CCT GCC CAA	340
Asn Asn. His	Gln Ser His	Gln Arg	Leu Thr Val	Asn Pro	Pro Ala Gln	
	10		15		20	
GGG GTC GCT TTG	ACT GGC	CGC CTA	AGG GTG	CCG GGG	GAT AAA TCC ATT	388
Gly Val	Ala Leu Thr	Gly Arg	Leu Arg	Val Pro	Gly Asp Lys Ser Ile	
	25		30		35	
TCC CAT CGG	GCC TTG	ATG TTG	GGG GCG	ATC GCC	ACC GGG GAA ACC ATT	436
Ser His	Arg Ala	Leu Met	Leu Gly	Ala Ile	Ala Thr Gly Gln Thr Ile	
	40		45		50	
ATC GAA GGG	CTA CTG TTG	GGG GAA	GAT CCC	CGT AGT	ACG GCC CAT TGC	484
Ile Gln	Gly Leu Leu	Gly Gln	Asp Pro	Arg Ser	Thr Ala His Cys	
	55		60		65	
					70	

Figure 21

SHEET 1 of 5

ATP ACC CCG GAG AAT GAA CGA TTG GTA ACC GCG GAA CCG GTA GCA GAT	1204
Ile Thr Pro Glu Asn Glu Arg Leu Val Thr Gly Glu Pro Val Ala Asp	
295	300
CGG GTT AGG GCA AGC CAT CTC CAG GGT TGC ACC TTC GGC GGC GAA	1252
Leu Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly Gly Glu	
315	320
ATP CCC CGA CTT ATP GAT GAA ATT CCC ATT TTG GCA GTG GCG GCG	1300
Ile Ile. Pro Arg Leu Ile Asp Glu Ile Pro Ile Leu Ala Val Ala Ala	
330	335
GCC TTT GCA GAG GGC ACT ACC CGC ATT GAA GAT GCC GCA GAA CTG AGG	1348
Ala Phe Ala Glu Gly Thr Thr Arg Ile Glu Asp Ala Ala Glu Leu Arg	
345	350
GTT AAA GAA AGC GAT CGC CTG GCG GCC ATT GCT TCG GAG TTG GGC AAA	1396
Val Lys Glu Ser Asp Arg Leu Ala Ala Ile Ala Ser Glu Leu Gly Lys	
360	365
ATG GGG GCC AAA GTC ACC GAA TTT GAT GAT GGC CTT GAA ATT CAA GCG	1444
Met Gly Ala Lys Val Thr Glu Phe Asp Asp Gly Leu Glu Ile Gln Gly	
375	380
UGA AGC CCG TTA CAA GGG GCC GAG GTG GAT AGC TTG ACG GAT CAT CGC	1492
Gly Ser Pro Leu Gln Gly Ala Glu Val Asp Ser Ser Leu Thr Asp His Arg	
395	400
	405

Figure 21

SHEET 4 of 5

004099-121599

ATT GCC ATG GCG TTG GCG ATC GCC GCT TTA GGT AGT GGG GGG CAA ACA	1540
Ile Ala Met Ala Leu Ala Ile Ala Ala Leu Gly Ser Gly Gln Thr	
410	
ATT ATT AAC CGG GCG GAA GCG GCC GCC ATT TCC TAT CCA GAA TTT TTT	1588
Ile Ile Asn Arg Ala Gln Ala Ala Ala Ile Ser Tyr Pro Gln Phe Phe	
425	
430	
435	
GGC ACG CTA GGG CAA GTT GCC CAA GGA TAAAGTTAGA AAAACTCCTG	1635
Gly Thr Leu Gly Gln Val Ala Gln Gly	
440	
445	
GGCGGTTCGTA AATGTTCCTA CCAAGTACT TTGGGTAA GGGCCAGCA AGTCTGCCA	1695
GGGTAAATTTA TCCGCAATTC ACCAATCGGC ATGAGCCGTA TCGTTCAAAC TGGTAATTC	1755
TCCCTTTAAT TCCTTAAAG CTCGCTTAA ACTGCCCAAC GTATCTCCGT AATGGCGAGT	1815
GAGTAAAGAT AATGGGGCCA AACGGCGATC GCCACGGGAA ATTAAGCCT GCATCACTGA	1875
CCACTTATTA CTTCGGGA	1894

Figure 21

SHEET 5 of 5

19404099-121599

TTTAAAAACCA ATGAGTAAAA AAATTATTTT TCTGGCACAC GCGCTTTT TTGCATTTT	60
CTCCCAATTTT TCCGGCACCA TAACGTTGGT TTTATAAAG GAAATG ATG ATG ACG	115
Met Met Thr	
1	
AAAT ATA TGG CAC ACC GCG CCC GTC TCT GCG CTT TCC GGC GAA ATA ACG	163
Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly Glu Ile Thr	
5 10 15	
ATA TGC GGC GAT AAA TCA ATG TCG CAT GCG GCC TTA TTA TTA GCA GCG	211
Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu Leu Ala Ala	
20 25 30 35	
TTA GCA GAA GGA CAA ACG GAA ATC CGC GGC TTT TTA GCG TGC GCG GAT	259
Leu Ala Glu Gly Gln Thr Glu Ile Arg Gly Phe Leu Ala Cys Ala Asp	
40 45 50	
TGT TTG GCG ACG CGG CAA GCA TTG CGC GCA TTA GGC GTT GAT ATT CAA	307
Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val Asp Ile Gln	
55 60 65	
AGA GAA AAA GAA ATA GTG ACG ATT CGC GGT GTG GGA TTT CTG GGT TTG	355
Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe Leu Gly Leu	
70 75 80	

Figure 22

SHEET 1 of 5

09461049 121599

CAG CCG CCG AAA GCA CCG TTA AAT ATG CAA AAC AGT GGC ACT AGC ATG 403
 Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly Thr Ser Met
 85 90 95

CGT TTA TTG GCA GGA ATT TTG GCA GCG CAG CGC TTT GAG AGC GTG TTA 451
 Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu Ser Val Leu
 100 105 110 115

TGC GGC GAT GAA TCA TTA GAA AAA CGT CCG ATG CAG CGC ATT ATT ACG 499
 Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg Ile Ile Thr
 120 125 130

CCG CTT GTG CAA ATG GGG GCA AAA ATT GTC AGT CAC AGC AAT TTT ACG 547
 Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser Asn Phe Thr
 135 140 145

GCG CCG TTA CAT ATT TCA GGA CGC CCG CTG ACC GGC ATT GAT TAC GCG 595
 Ala Pro Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile Asp Tyr Ala
 150 155 160

TTA CCG CTT CCC AGC GCG CAA TTA AAA AGT TGC CTT ATT TTG GCA GGA 643
 Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile Leu Ala Gly
 165 170 175

TTA TTG GCT GAC GGT ACC ACG CGG CTG CAT ACT TGC GGC ATC AGT CGC 691
 Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly Ile Ser Arg
 180 185 190 195

GAC CAC ACC GAA CGC ATG TTG CCG CTT TTT GGT GGC GCA CTT GAG ATC 739
 Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala Leu Glu Ile 210
 200

AAG AAA GAG CAA ATA ATC GTC ACC GGT GGA CAA AAA TTG CAC GGT TGC 787
 Lys Lys Glu Gln Ile Ile Val Thr Gly Gly Gln Lys Leu His Gly Cys 225
 215 220

GTC CTT GAT ATT GTC GGC GAT TTG TCG GCG GCG GCG TTT TTT ATG GTT 835
 Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Ala Phe Phe Met Val 240
 230 235

GCG GCT TTG ATT GCG CCG CCG GCG GAA GTC GTT ATT CGT AAT GTC GGC 883
 Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Val Ile Arg Asn Val Gly 255
 245 250

ATT AAT CCG ACG CCG GCG GCA ATC ATT ACT TTG TTG CAA AAA ATG GGC 931
 Ile Asn Pro Thr Arg Ala Ala Ile Ile Thr Leu Leu Gln Lys Met Gly 275
 260 265 270

GGA CCG ATT GAA TTG CAT CAT CAG CGC TTT TGG GGC GCC GAA CCG GTG 979
 Gly Arg Ile Glu, Leu His His Gln Arg Phe Trp Gly Ala Glu Pro Val 290
 280 285

GCA GAT ATT GTT GTT TAT CAT TCA AAA TTG CCG GGC ATT ACG GTG GCG 1027
 Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile Thr Val Ala 305
 295 300

Figure 22

SHEET 3 of 5

49464039-121699

CCG GAA TGG ATT GCC AAC GCG ATT GAT GAA TTG CCG ATT TTT TTT ATT 1075
 Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile Phe Phe Ile
 310 315 320

GCG GCA GCT TGC GCG GAA GGG ACG ACT TTT GTG GGC AAT TTG TCA GAA 1123
 Ala Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn Leu Ser Glu
 325 330 335

TTG CGT GTG AAA GAA TCG GAT CGT TTA GCG GCG ATG GCG CAA AAT TTA 1171
 Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala Glu Asn Leu
 340 345 350 355

CAA ACT TTG GGC GTG GCG TGC GAC GTT GGC GCC GAT TTT ATT CAT ATA 1219
 Glu Thr Leu Gly Val Ala Cys Asp Val Gly Ala Asp Phe Ile His Ile
 360 365 370

TAT GGA AGA AGC GAT CCG CAA TTT TTA CCG GCG CCG GTG AAC AGT TTT 1267
 Tyr Gly Arg Ser Asp Arg Glu Phe Leu Pro Ala Arg Val Asn Ser Phe
 375 380 385

GGC GAT CAT CCG ATT CCG ATG AGT TTG GCG GTG GCA GGT GTG CGC GCG 1315
 Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly Val Arg Ala
 390 395 400

GCA GGT GAA TTA TTG ATT GAT GAC GCG GCG GTG GCG GCG GTT TCT ATG 1363
 Ala Gly Glu Leu Leu Ile Asp Asp Gly Ala Val Ala Val Val Ser Met
 405 410 415

Figure 22

SHEET 4 of 5

05454099-1234567

UCC CAA TTT CGC GAT TTTT GCC GCC GCA ATT GGT ATG AAT GTA GCA GAA	1411
Pro Gln Phe Arg Asp Phe Ala Ala Ala Ile Gly Met Asn Val Gly Glu	
420	
425	
430	
435	

AAA GAT GCG AAA AAT TGT CAC GAT TGATGCTCCT AGCGGTGTG GAAAGGCAC	1465
Lys Asp Ala Lys Asn Cys His Asp	
440	

GGTGGCCCAA GCTT	1479
-----------------	------

094640992121699

	1	40
PG2982MS HSASPKPATA RRSEALTGEI RIPGDKSISH	
LBAAMS HSASPKPATA RRSEALTGEI RIPGDKSISH	
Agrobacterium CP4MS HGASSRPATA RKSSGLSGTV RIPGDKSISH	
Synechocystis sp. PCC6803	MALLSLNNHQ SHQRLTVNPP AQGVALTGRL RVPGDKSISH	
B. subtilisMCR DKVQTLHGEI HIPGDKSISH	
D. nodosusMTNINWHT APVSALSGEI TICGDKSM SH	
S. aureusMVNEQII DISGPLKEI EVPGDKSMTH	
Consensus	-----L-G-- -I-GDKS--H	
PG2982	41	80
LBAA	RSFMFGGLAS GETRITGLLE GEDVINTGRA MQAMGAKI.R	
Agrobacterium CP4	RSFMFGGLAS GETRITGLLE GEDVINTGRA MQAMGAKI.R	
Synechocystis sp. PCC6803	RSFMFGGLAS GETRITGLLE GEDVINTGKA MQAMGARI.R	
B. subtilis	RALMLGAIAAT GETTIEGLL GEDPRSTAHC FRAMGAEISE	
D. nodosus	RSVMFGALAA GTTVKNFLP GADCLSTIDC FRKMGVHI.E	
S. aureus	RALLLALAE GQTEIRGFLA CADCLATRQA LRALGVDI.Q	
Consensus	RAIMLASLAE GVSTIYKPLL GEDCRRTMDI FRHLGVEI.K	
	R--MF--A- G---I---L- --D---T--- --MG--I--	
PG2982	81	120
LBAA	KEGDVWIING VNGCCLLOPE AALDFGNAGT GARLTMGLVG	
Agrobacterium CP4	KEGDVWIING VNGCCLLOPE AALDFGNAGT GARLTMGLVG	
Synechocystis sp. PCC6803	KEGDTWIIDG VNGGCLLAP EAPLDFGNAT GCRLTMGLVG	
B. subtilis	LNSEKIIVQG RGLGQLQEPS TVLDAGNSGT TMRMLGLLA	
D. nodosus	QSSSDVVIHG KGIDALKEPE SLDDVNSGT TIRMLGILA	
S. aureus	REKEIVTIRG VGFLGLQPPK APLNMQNSGT SMRLLAGILA	
Consensus	EDDEKLVTTS PGYQ.VNTPH QVLYTGNSGT TTRLLAGLLS	
	-----I-- -G-----P- --L---N--T --RL--G---	

Figure 23 SHEET 1 of 4

0044079.121599

	121		160
PG2982	TY.DMKTSEI	GDASLSKRPM	GRVLNPLREM
LBAA	TY.DMKTSEI	GDASLSKRPM	GRVLNPLREM
Agrobacterium CP4	VY.DFDSTFI	GDASLTKRPM	GRVLNPLREM
Synechocystis sp. PCC6803	GQKDCLEFVT	GDDSLRHRPM	SRVIOPLQOM
B. subtilis	G.RPFYSAVA	GDESIKRPM	KRVTEPLKKM
D. nodosus	AQR.FESVLC	GDESLEKRPM	QRIITPLVQM
S. aureus	GLGN.ESVLS	GDVSIKRRPM	DRVLRPLKM
Consensus	GD-S--RPM	-RV--PL--M	----I-----
	161		200
PG2982	RMPLTLIGPK	TANPITYRVP	MASAQVKSAY
LBAA	RMPLTLIGPK	TANPITYRVP	MASAQVKSAY
Agrobacterium CP4	RLPVTLRGPK	TPTPITYRVP	MASAQVKSAY
Synechocystis sp. PCC6803	KFAPLAVQGS	QLKPIHYHSP	IASAQVKSCL
B. subtilis	EFTPLSVSGA	SLKGIDYVSP	VASAQIKSAV
D. nodosus	T.APLHISGR	PLTGIDYALP	LPSAQLKSCS
S. aureus	.YTPLIIKPS	VIKGINYQME	VASAQVKSAI
Consensus	-----I-Y----	--SAO-KS--	-LA-L-----
	201		240
PG2982	TTVIEPVMTR	DHTEKMLQGFGADLT
LBAA	TTVIEPVMTR	DHTEKMLQGFGADLT
Agrobacterium CP4	TTVIEPIPTR	DHTEKMLQGFGANLT
Synechocystis sp. PCC6803	TTVTEPALSR	DHSERMLQAFGAKLT
B. subtilis	TTVTEPHKSR	DHTEKMLSAFGVKLS
D. nodosus	TRLHTCGISR	DHTEKMLPLFGALE
S. aureus	TIKELDVS	NHTEKMFKEH	NIPIEAGLS
Consensus	T-----R-H-E-ML--F	-----L-	-----V--

Figure 23

	241		280
PG2982	IRITGQGLV	GQTIDVPGDP	SSTAFLVAA
LBAA	IRITGQGLV	GQTIDVPGDP	SSTAFLVAA
Agrobacterium CP4	IRLEGRGLT	GQVIDVPGDP	SSTAFLVAA
Synechocystis sp. PCC6803	.TVHGPAHLT	GQRVVVPEDI	SSAFLVAA
B. subtilis	.SIAGGQKLT	AADIFVPGDI	SSAFLAAG
D. nodosus	.IVTGGQKLH	GCVLIDVGD	SSAFLVAA
S. aureus	IKPAD.....	..FHVPGDI	SSAFLVAA
Consensus	-----V-GD-	S--AF--A-	-----
PG2982	281		320
LBAA	RNVLMNPTRT	GLILTLQEMG	ADIEVLNARL
Agrobacterium CP4	RNVLMNPTRT	GLILTLQEMG	ADIEVLNARL
Synechocystis sp. PCC6803	LNVLNPTRT	GIILTLQEMG	ADIEVINPRL
B. subtilis	ENVGINPTRT	GVLVLAQMG	ADITPENERL
D. nodosus	KNVGLNPTRT	GIIDVLQNMG	AKLEIKPSAD
S. aureus	RNVGINPTRA	AIITLLQKMG	GRIELHHQRF
Consensus	HNVGINQTRS	GIIDIVEKMG	GNIQLFNQT.
	-NV--N-TR-	-----MG	-----E-----
PG2982	321		360
LBAA	VR.ASKLKV	VPPERAPSM	IDEXPVLAIA
Agrobacterium CP4	VR.ASKLKV	VPPERAPSM	IDEXPVLAIA
Synechocystis sp. PCC6803	VR.SSTLKV	TVPEDRAPSM	IDEXPVLAIA
B. subtilis	VR.ASHLQGC	TFGGEIIPRL	IDEIPILAVA
D. nodosus	IE.TSSLKAV	EIGGDIIPRL	IDEIPIALA
S. aureus	VY.HSKLRGI	TVAPEWIANA	IDELPIFFIA
Consensus	IQYTPMLQPI	TIEGELVPKA	IDELPVIALA
	V-----L---	-----E-----	IDE-PI-----A-G-----

Figure 23

SHEET 3 of 4

669727 65049460

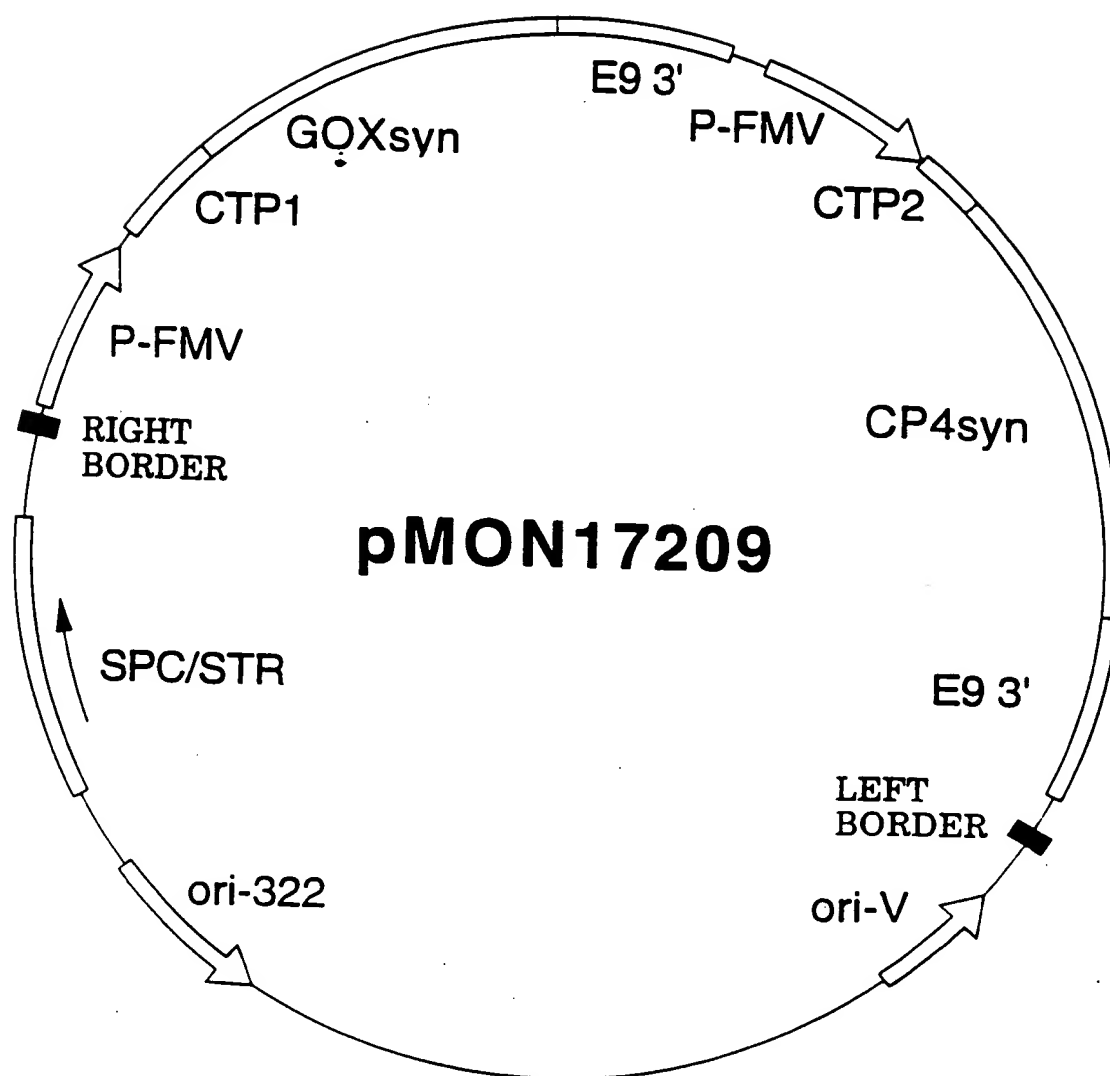


Figure 24

669721 66049460

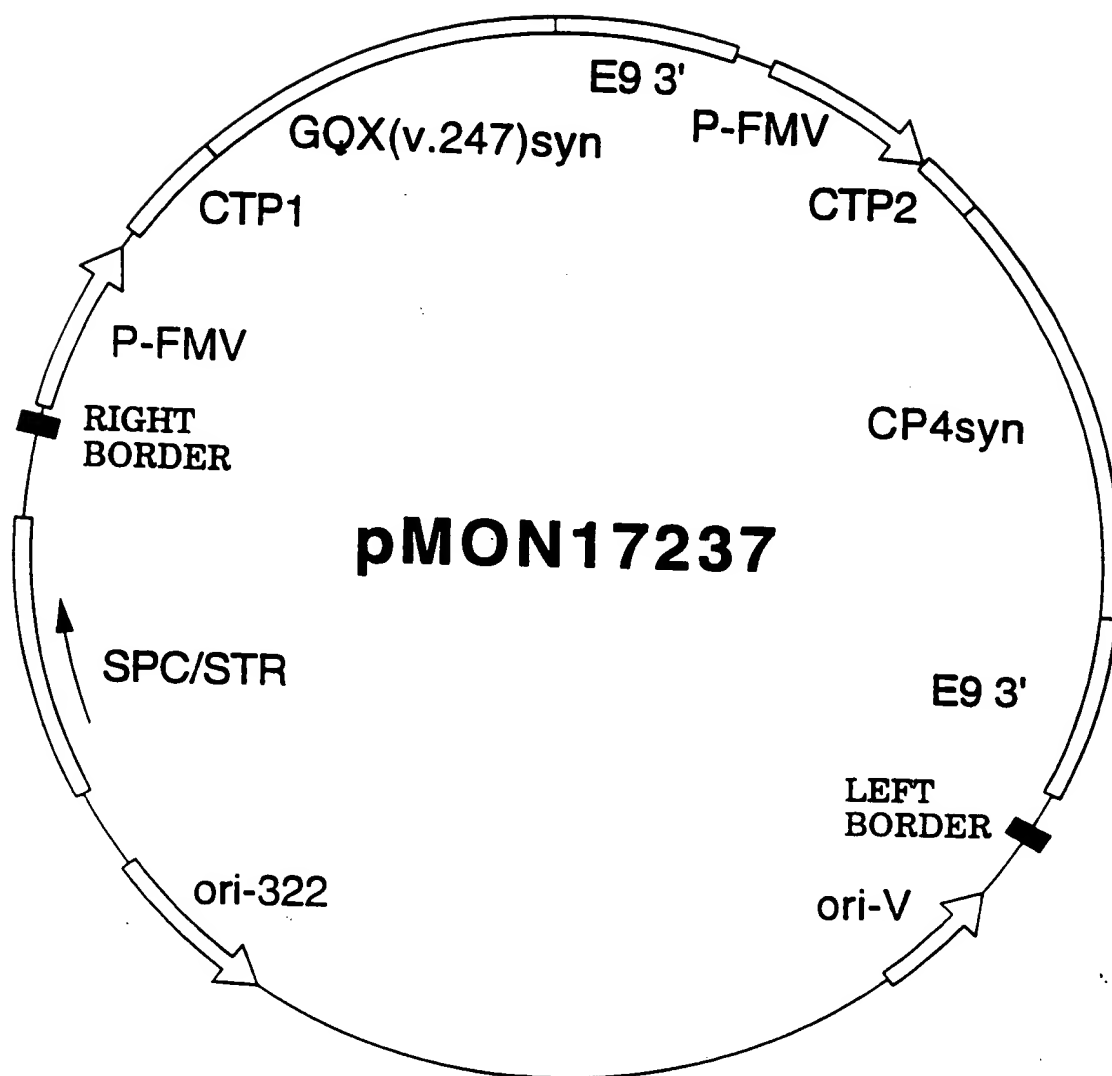


Figure 25